CLAIMS

What is claimed is:

1. An interactive display system comprising:

a database of comparative genomic data from at least two species; and

a viewer adapted to integrate the comparative genomic data.

2. An interactive display system according to claim 1, further comprising an ortholog identifier adapted to identify orthologous genes of the two or more species.

3. An interactive display system according to claim 1, wherein the comparative genomic data comprises syntenic anchors and syntenic blocks from the two or more species.

4. An interactive display system according to claim 3, wherein the two species include mouse and human.

5. An interactive display system according to claim 4, further comprising comparative genomic data from at least three species.

6. An interactive display system according to claim 5 wherein the at least three species include rat.

7.   An interactive display system according to claim 1, wherein the viewer comprises a map viewer which shows genomic sequence information of the two or more species with markers therein.

8.   An interactive display system according to claim 1, wherein the viewer comprises a TA viewer which shows at least one contig and fragments used to generate the contig.

9.   An interactive display system according to claim 1, wherein the viewer comprises an evidence viewer which provides annotation information associated with transcribed regions of the genomic data from the at least two species.

10.   An interactive display system according to claim 1, wherein the viewer comprises a synteny viewer which shows syntenic relationships between the genomic sequence data of the at least two species.

11.   An interactive display system according to claim 1, wherein the viewer comprises a multiple sequence alignment viewer which shows multiple sequence alignments of genomic sequences of the at least two species.

12.   An interactive display system according to claim 1, wherein the viewer comprises a trace viewer which shows single nucleotides in genomic sequences of the at least two species.

13.   An interactive display system according to claim 1, wherein said viewer comprises at least two viewer components selected from the group consisting of:

(a)   a map viewer which shows genomic sequence information of the two or more species with markers therein;

(b)   a TA viewer which shows at least one contig and fragments used to generate the contig;

(c)   an evidence viewer which provides annotation information associated with transcribed regions of the genomic data from the at least two species;

(d)   a synteny viewer which shows syntenic relationships between the genomic sequence data of the at least two species;

(e)   a multiple sequence alignment viewer which shows multiple sequence alignments of genomic sequences of the at least two species; and

(f)   a trace viewer which shows single nucleotides in genomic sequences of the at least two species.

14.   An interactive display system according to claim 13, wherein said viewer is adapted to allow a user to select viewer components, thereby averting display to the user and viewer interaction with unselected viewer components .

15.   An interactive display system according to claim 13, wherein said viewer comprises at least three viewer components selected from the group.

16.   An interactive display system according to claim 13, wherein said viewer comprises at least four viewer components selected from the group.

17.   An interactive display system according to claim 13, wherein said viewer comprises at least five viewer components selected from the group.

18.   An interactive display system according to claim 13, wherein said viewer comprises at least six viewer components selected from the group.

19.   An interactive display system according to claim 1, wherein said database of comparative genomic data comprises susbstantially complete genomic sequence of the two or more species.

20.   An interactive display system according to claim 1, wherein the system is provided in a stand-alone format.

21.   An interactive display system according to claim 1, wherein the system is provided in a web-based format.

22.   A method for generating a database of genomic sequences of two or more species which identifies orthologous genomic regions between the two or more species, comprising:

performing at least one BLAST search using the genomic sequences of each of the two or more species against the genomic sequences of each of the other of the two or more species;

selecting best putative ortholog matches; and

identifying best ortholog matches among the best putative ortholog matches.

23.   A method according to claim 22 further comprising identifying syntenic anchors and syntenic block to facilitate selecting the best putative ortholog matches.

24. A method for identifying orthologous genomic regions between two or more species, comprising:

performing at least one BLAST search using each of the two or more species against each of the other of the two or more species;

selecting best putative ortholog matches; and

identifying best ortholog matches among the best putative ortholog matches.

25. A method according to claim 24, further comprising identifying syntenic anchors and syntenic block to facilitate selecting the best putative ortholog matches.

26. A method for communicating orthologous genomic regions between at least two species to a user, comprising:

accessing comparative genomic data from at least two species; and

providing a viewer adapted to integrate the comparative genomic data and present it to the user.

27. A method according to claim 26, further comprising identifying orthologous genes of the two or more species.

28.   A method according to claim 27, further comprising:

performing at least one BLAST search using genomic data from at least one of the two species against genomic data of each of the other at least two species;

selecting best putative ortholog matches; and

identifying best ortholog matches among the best putative ortholog matches.

29.   A method according to claim 28, further comprising identifying syntenic anchors and syntenic block to facilitate selecting the best putative ortholog matches.

30.   A method according to claim 26, further comprising providing a map viewer which shows genomic sequence information of the two or more species with markers therein.

31.   A method according to claim 26, further comprising providing a TA viewer which shows at least one contig and fragments used to generate the contig.

32.   A method according to claim 26, further comprising providing an evidence viewer which provides annotation information associated with transcribed regions of the genomic data from the at least two species.

33.   A method according to claim 26, further comprising providing a synteny viewer which shows syntenic relationships between the genomic sequence data of the at least two species.

34.   A method according to claim 26, further comprising providing a multiple sequence alignment viewer which shows multiple sequence alignments of genomic sequences of the at least two species.

35.   A method according to claim 26, further comprising providing a trace viewer which shows single nucleotides in genomic sequences of the at least two species.